



IPE

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ENCODING THE SAME, AND USES THEREOF**MAIL STOP PCT**

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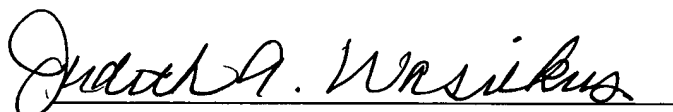
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Alexandria, VA 22313-1450

VERIFIED STATEMENT UNDER 37 CFR §1.821(f)

I, Judith A. Wasilkus, declare that I personally prepared the paper and the computer-readable copy of the Sequence Listing filed herewith for the above-identified application and that the content of both is the same.

I further declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of The United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Date: May 23, 2003
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60142814.doc

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<120> VARIANTS OF THE GAMMA CHAIN OF AMPK, DNA SEQUENCES ENCODING
THE SAME, AND USES THEREOF

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Lys	Pro	Leu	Val	Ser	Ile	Ser	Pro	Asn	Asp	Ser	Leu	Phe	Glu	Ala	Val	
			260					265					270			
tac	gcc	ctc	atc	aag	aac	cgg	atc	cac	cgc	ctg	ccg	gtc	ctg	gac	cct	864
Tyr	Ala	Leu	Ile	Lys	Asn	Arg	Ile	His	Arg	Leu	Pro	Val	Leu	Asp	Pro	
			275				280					285				
gtc	tcc	ggg	gct	gtg	ctc	cac	atc	ctc	aca	cat	aag	cgg	ctt	ctc	aag	912
Val	Ser	Gly	Ala	Val	Leu	His	Ile	Leu	Thr	His	Lys	Arg	Leu	Leu	Lys	
		290					295				300					
ttc	ctg	cac	atc	ttt	ggc	acc	ctg	ctg	ccc	cgg	ccc	tcc	ttc	ctc	tac	960
Phe	Leu	His	Ile	Phe	Gly	Thr	Leu	Leu	Pro	Arg	Pro	Ser	Phe	Leu	Tyr	
305					310					315					320	
cgc	acc	atc	caa	gat	ttg	ggc	atc	ggc	aca	ttc	cga	gac	ttg	gcc	gtg	1008
Arg	Thr	Ile	Gln	Asp	Leu	Gly	Ile	Gly	Thr	Phe	Arg	Asp	Leu	Ala	Val	
				325					330					335		
gtg	ctg	gaa	acg	gcg	ccc	atc	ctg	acc	gca	ctg	gac	atc	ttc	gtg	gac	1056
Val	Leu	Glu	Thr	Ala	Pro	Ile	Leu	Thr	Ala	Leu	Asp	Ile	Phe	Val	Asp	
			340					345					350			
cgg	cgt	gtg	tct	gcg	ctg	cct	gtg	gtc	aac	gaa	act	gga	cag	gta	gtg	1104
Arg	Arg	Val	Ser	Ala	Leu	Pro	Val	Val	Asn	Glu	Thr	Gly	Gln	Val	Val	
		355					360					365				
ggc	ctc	tac	tct	cgc	ttt	gat	gtg	atc	cac	ctg	gct	gcc	caa	caa	aca	1152
Gly	Leu	Tyr	Ser	Arg	Phe	Asp	Val	Ile	His	Leu	Ala	Ala	Gln	Gln	Thr	
		370				375					380					
tac	aac	cac	ctg	gac	atg	aat	gtg	gga	gaa	gcc	ctg	agg	cag	cgg	aca	1200
Tyr	Asn	His	Leu	Asp	Met	Asn	Val	Gly	Glu	Ala	Leu	Arg	Gln	Arg	Thr	
385					390					395					400	
ctg	tgt	ctg	gaa	ggc	gtc	ctt	tcc	tgc	cag	ccc	cac	gag	acc	ttg	ggg	1248
Leu	Cys	Leu	Glu	Gly	Val	Leu	Ser	Cys	Gln	Pro	His	Glu	Thr	Leu	Gly	
				405					410					415		
gaa	gtc	att	gac	cgg	att	gtc	cgg	gaa	cag	gtg	cac	cgc	ctg	gtg	ctc	1296
Glu	Val	Ile	Asp	Arg	Ile	Val	Arg	Glu	Gln	Val	His	Arg	Leu	Val	Leu	
			420					425					430			

tga gaaccttga acctttgctc tcaggccacc tggcacacct ggaagccagt 1445
465

gaagggagcc	gtggactcag	ctctcacttc	ccctcagccc	cacttgctgg	tctggctctt	1505
gttcaggtag	gctccgcccg	gggcccctgg	cctcagcatt	agcccctcag	tctccctggg	1565
caccagatc	tcagactggg	gcaccctgaa	gatgggagtg	gccagctta	tagctgagca	1625
gccttgtaaa	atctaccagc	atcaagactc	actgtgggac	cactgctttg	tcccattctc	1685
agctgaaatg	atggagggcc	tcataagagg	ggtggacagg	gcctggagta	gaggccagat	1745
cagtgacgtg	ccttcaggac	ctccggggag	ttagagctgc	cctctctcag	ttcagttccc	1805
ccctgctgag	aatgtccctg	gaaggaagcc	agttaataaa	ccttggttgg	atggaatttg	1865
gagagtcg						1873

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<210> 28
<211> 464
<212> PRT
<213> Sus scrofa
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<400> 28															
Met	Ser	Phe	Leu	Glu	Gln	Gly	Glu	Ser	Arg	Ser	Trp	Pro	Ser	Arg	Ala
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Val	Thr	Thr	Ser	Ser	Glu	Arg	Ser	His	Gly	Asp	Gln	Gly	Asn	Lys	Ala
			20					25					30		
Ser	Arg	Trp	Thr	Arg	Gln	Glu	Asp	Val	Glu	Glu	Gly	Gly	Pro	Pro	Gly
		35					40					45			
Pro	Arg	Glu	Gly	Pro	Gln	Ser	Arg	Pro	Val	Ala	Glu	Ser	Thr	Gly	Gln
	50					55					60				
Glu	Ala	Thr	Phe	Pro	Lys	Ala	Thr	Pro	Leu	Ala	Gln	Ala	Ala	Pro	Leu
65					70					75					80
Ala	Glu	Val	Asp	Asn	Pro	Pro	Thr	Glu	Arg	Asp	Ile	Leu	Pro	Ser	Asp
				85					90					95	
Cys	Ala	Ala	Ser	Ala	Ser	Asp	Ser	Asn	Thr	Asp	His	Leu	Asp	Leu	Gly
			100					105				110			
Ile	Glu	Phe	Ser	Ala	Ser	Ala	Ala	Ser	Gly	Asp	Glu	Leu	Gly	Leu	Val
		115					120					125			
Glu	Glu	Lys	Pro	Ala	Pro	Cys	Pro	Ser	Pro	Glu	Val	Leu	Leu	Pro	Arg
	130					135					140				
Leu	Gly	Trp	Asp	Asp	Glu	Leu	Gln	Lys	Pro	Gly	Ala	Gln	Val	Tyr	Met
145				150						155					160
His	Phe	Met	Gln	Glu	His	Thr	Cys	Tyr	Asp	Ala	Met	Ala	Thr	Ser	Ser
				165					170					175	

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Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe
      180                      185                      190
Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys
      195                      200                      205
Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val
      210                      215                      220
Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu
      225                      230                      235                      240
Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe
      245                      250                      255
Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val
      260                      265                      270
Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro
      275                      280                      285
Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys
      290                      295                      300
Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr
      305                      310                      315                      320
Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val
      325                      330                      335
Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp
      340                      345                      350
Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val
      355                      360                      365
Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr
      370                      375                      380
Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr
      385                      390                      395                      400
Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly
      405                      410                      415
Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu
      420                      425                      430
Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile
      435                      440                      445
Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala
      450                      455                      460

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<210> 29
<211> 2115
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (1)..(1395)

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<400> 29
atg agc ttc cta gag caa gaa aac agc agc tca tgg cca tca cca gct   48
Met Ser Phe Leu Glu Gln Glu Asn Ser Ser Ser Trp Pro Ser Pro Ala
  1                      5                      10                      15

gtg acc agc agc tca gaa aga atc cgt ggg aaa cgg agg gcc aaa gcc   96
Val Thr Ser Ser Ser Glu Arg Ile Arg Gly Lys Arg Arg Ala Lys Ala
      20                      25                      30

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ttg aga tgg aca agg cag aag tcg gtg gag gaa ggg gag cca cca ggt	144
Leu Arg Trp Thr Arg Gln Lys Ser Val Glu Glu Gly Glu Pro Pro Gly	
35 40 45	
cag ggg gaa ggt ccc cgg tcc agg cca act gct gag tcc acc ggg ctg	192
Gln Gly Glu Gly Pro Arg Ser Arg Pro Thr Ala Glu Ser Thr Gly Leu	
50 55 60	
gag gcc aca ttc ccc aag acc aca ccc ttg gct caa gct gat cct gcc	240
Glu Ala Thr Phe Pro Lys Thr Thr Pro Leu Ala Gln Ala Asp Pro Ala	
65 70 75 80	
ggg gtg ggc act cca cca aca ggg tgg gac tgc ctc ccc tct gac tgt	288
Gly Val Gly Thr Pro Pro Thr Gly Trp Asp Cys Leu Pro Ser Asp Cys	
85 90 95	
aca gcc tca gct gca ggc tcc agc aca gat gat gtg gag ctg gcc acg	336
Thr Ala Ser Ala Ala Gly Ser Ser Thr Asp Asp Val Glu Leu Ala Thr	
100 105 110	
gag ttc cca gcc aca gag gcc tgg gag tgt gag cta gaa ggc ctg ctg	384
Glu Phe Pro Ala Thr Glu Ala Trp Glu Cys Glu Leu Glu Gly Leu Leu	
115 120 125	
gaa gag agg cct gcc ctg tgc ctg tcc ccg cag gcc cca ttt ccc aag	432
Glu Glu Arg Pro Ala Leu Cys Leu Ser Pro Gln Ala Pro Phe Pro Lys	
130 135 140	
ctg ggc tgg gat gac gaa ctg cgg aaa ccc ggc gcc cag atc tac atg	480
Leu Gly Trp Asp Asp Glu Leu Arg Lys Pro Gly Ala Gln Ile Tyr Met	
145 150 155 160	
cgc ttc atg cag gag cac acc tgc tac gat gcc atg gca act agc tcc	528
Arg Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser	
165 170 175	
aag cta gtc atc ttc gac acc atg ctg gag atc aag aag gcc ttc ttt	576
Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe	
180 185 190	
gct ctg gtg gcc aac ggt gtg cgg gca gcc cct cta tgg gac agc aag	624
Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys	
195 200 205	
aag cag agc ttt gtg ggg atg ctg acc atc act gac ttc atc ctg gtg	672
Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val	
210 215 220	
ctg cat cgc tac tac agg tcc ccc ctg gtc cag atc tat gag att gaa	720
Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu	
225 230 235 240	
caa cat aag att gag acc tgg agg gag atc tac ctg caa ggc tgc ttc	768
Gln His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe	
245 250 255	

aag cct ctg gtc tcc atc tct cct aat gat agc ctg ttt gaa gct gtc	816
Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val	
260 265 270	
tac acc ctc atc aag aac cgg atc cat cgc ctg cct gtt ctt gac ccg	864
Tyr Thr Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro	
275 280 285	
gtg tca ggc aac gta ctc cac atc ctc aca cac aaa cgc ctg ctc aag	912
Val Ser Gly Asn Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys	
290 295 300	
ttc ctg cac atc ttt ggt tcc ctg ctg ccc cgg ccc tcc ttc ctc tac	960
Phe Leu His Ile Phe Gly Ser Leu Leu Pro Arg Pro Ser Phe Leu Tyr	
305 310 315 320	
cgc act atc caa gat ttg ggc atc ggc aca ttc cga gac ttg gct gtg	1008
Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val	
325 330 335	
gtg ctg gag aca gca ccc atc ctg act gca ctg gac atc ttt gtg gac	1056
Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp	
340 345 350	
cgg cgt gtg tct gca ctg cct gtg gtc aac gaa tgt ggt cag gtc gtg	1104
Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Cys Gly Gln Val Val	
355 360 365	
ggc ctc tat tcc cgc ttt gat gtg att cac ctg gct gcc cag caa acc	1152
Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr	
370 375 380	
tac aac cac ctg gac atg agt gtg gga gaa gcc ctg agg cag agg aca	1200
Tyr Asn His Leu Asp Met Ser Val Gly Glu Ala Leu Arg Gln Arg Thr	
385 390 395 400	
cta tgt ctg gag gga gtc ctt tcc tgc cag ccc cac gag agc ttg ggg	1248
Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Ser Leu Gly	
405 410 415	
gaa gtg atc gac agg att gct cgg gag cag gta cac agg ctg gtg cta	1296
Glu Val Ile Asp Arg Ile Ala Arg Glu Gln Val His Arg Leu Val Leu	
420 425 430	
gtg gac gag acc cag cat ctc ttg ggc gtg gtc tcc ctc tcc gac atc	1344
Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile	
435 440 445	
ctt cag gca ctg gtg ctc agc cct gct ggc atc gat gcc ctc ggg gcc	1392
Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala	
450 455 460	
tga gaagatctga gtcttcaatc ccaagccaac tgcacactgg aagccaatga	1445

aggaattgag aacagcttca tttccccaac cccaatttgc tggttcagct atgattcagg 1505
 cttcttcagc cttccaaaat tgcctttgcc ttacttgtgc tcccagaacc cttcgggcat 1565
 gcccagtgc ccatgggatg atgaaattaa ggagaacagc tgagtcaagc ttggaggtcc 1625
 ctgaaccaga ggcactagga ttaccccagg gccatctgtg ctccatgccc gcccatcccc 1685
 ttgccgcctg actgggtcgg atggccccag tgggtttagt cagggcttct ggattcctcg 1745
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 tgcatttcag gggccaccat ggagcagccg ttatttatag aactgcctgt tggaggtggg 1925
 gagtccctcc tccattcttg tccagaaaac tccttagctc tcgcagtgc ccatgttctt 1985
 agtctccagg gatggatggc cttgtatatg gaccctgag aatgagcaat tgagaaaaca 2045
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 atttgacctg 2115

<210> 30
 <211> 464
 <212> PRT
 <213> Homo sapiens

<400> 30
 Met Ser Phe Leu Glu Gln Glu Asn Ser Ser Ser Trp Pro Ser Pro Ala
 1 5 10 15
 Val Thr Ser Ser Ser Glu Arg Ile Arg Gly Lys Arg Arg Ala Lys Ala
 20 25 30
 Leu Arg Trp Thr Arg Gln Lys Ser Val Glu Glu Gly Glu Pro Pro Gly
 35 40 45
 Gln Gly Glu Gly Pro Arg Ser Arg Pro Thr Ala Glu Ser Thr Gly Leu
 50 55 60
 Glu Ala Thr Phe Pro Lys Thr Thr Pro Leu Ala Gln Ala Asp Pro Ala
 65 70 75 80
 Gly Val Gly Thr Pro Pro Thr Gly Trp Asp Cys Leu Pro Ser Asp Cys
 85 90 95
 Thr Ala Ser Ala Ala Gly Ser Ser Thr Asp Asp Val Glu Leu Ala Thr
 100 105 110
 Glu Phe Pro Ala Thr Glu Ala Trp Glu Cys Glu Leu Glu Gly Leu Leu
 115 120 125
 Glu Glu Arg Pro Ala Leu Cys Leu Ser Pro Gln Ala Pro Phe Pro Lys
 130 135 140
 Leu Gly Trp Asp Asp Glu Leu Arg Lys Pro Gly Ala Gln Ile Tyr Met
 145 150 155 160
 Arg Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser
 165 170 175
 Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe
 180 185 190
 Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys
 195 200 205

Lys	Gln	Ser	Phe	Val	Gly	Met	Leu	Thr	Ile	Thr	Asp	Phe	Ile	Leu	Val
210						215					220				
Leu	His	Arg	Tyr	Tyr	Arg	Ser	Pro	Leu	Val	Gln	Ile	Tyr	Glu	Ile	Glu
225					230					235					240
Gln	His	Lys	Ile	Glu	Thr	Trp	Arg	Glu	Ile	Tyr	Leu	Gln	Gly	Cys	Phe
			245					250						255	
Lys	Pro	Leu	Val	Ser	Ile	Ser	Pro	Asn	Asp	Ser	Leu	Phe	Glu	Ala	Val
		260				265					270				
Tyr	Thr	Leu	Ile	Lys	Asn	Arg	Ile	His	Arg	Leu	Pro	Val	Leu	Asp	Pro
275					280						285				
Val	Ser	Gly	Asn	Val	Leu	His	Ile	Leu	Thr	His	Lys	Arg	Leu	Leu	Lys
290				295						300					
Phe	Leu	His	Ile	Phe	Gly	Ser	Leu	Leu	Pro	Arg	Pro	Ser	Phe	Leu	Tyr
305				310					315						320
Arg	Thr	Ile	Gln	Asp	Leu	Gly	Ile	Gly	Thr	Phe	Arg	Asp	Leu	Ala	Val
			325					330						335	
Val	Leu	Glu	Thr	Ala	Pro	Ile	Leu	Thr	Ala	Leu	Asp	Ile	Phe	Val	Asp
		340					345					350			
Arg	Arg	Val	Ser	Ala	Leu	Pro	Val	Val	Asn	Glu	Cys	Gly	Gln	Val	Val
	355					360					365				
Gly	Leu	Tyr	Ser	Arg	Phe	Asp	Val	Ile	His	Leu	Ala	Ala	Gln	Gln	Thr
370				375						380					
Tyr	Asn	His	Leu	Asp	Met	Ser	Val	Gly	Glu	Ala	Leu	Arg	Gln	Arg	Thr
385				390					395						400
Leu	Cys	Leu	Glu	Gly	Val	Leu	Ser	Cys	Gln	Pro	His	Glu	Ser	Leu	Gly
			405					410						415	
Glu	Val	Ile	Asp	Arg	Ile	Ala	Arg	Glu	Gln	Val	His	Arg	Leu	Val	Leu
		420				425						430			
Val	Asp	Glu	Thr	Gln	His	Leu	Leu	Gly	Val	Val	Ser	Leu	Ser	Asp	Ile
	435					440					445				
Leu	Gln	Ala	Leu	Val	Leu	Ser	Pro	Ala	Gly	Ile	Asp	Ala	Leu	Gly	Ala
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<210> 31
 <211> 2022
 <212> DNA
 <213> Sus scrofa

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 agcagcctcg ggggacctaa gcatcaagag atgagcttcc tagagcaagg agagagccgt 180
 tcatggccat cccgagctgt aaccaccagc tcagaaagaa gccatgggga ccaggggaac 240
 aaggcctcta gatggacaag gcaggaggat gtagaggaag gggggcctcc gggcccagg 300
 gaagggtccc agtccaggcc agttgctgag tccaccgggc aggaggccac attccccaa 360
 gccacaccct tggcccaagc cgctcccttg gccgaggtgg acaaccccc aacagagcgg 420
 gacatcctcc cctctgactg tgcagcctca gcctccgact ccaacacaga ccatctggat 480
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 aagccagccc cgtgccccca cccagagggtg ctgttaccca ggctgggctg ggatgatgag 600
 ctgcagaagc cgggggccca ggtctacatg cacttcatgc aggagcacac ctgctacgat 660
 gccatggcga ccagctccaa actggtcatc ttcgacacca tgctggagat caagaaggcc 720
 ttctttgccc tgggtggcaa cggcggtccga gcggcacctt tgtgggacag caagaagcag 780
 agcttcgtgg ggatgctgac catcacagac ttcattcttg tgctgcaccg ctattacagg 840
 tccccctgg tccagatcta cgagattgaa gaacataaga ttgagacctg gagggagatc 900
 taccttcaag gctgcttcaa gcctctgggtc tccatctctc ccaatgacag cctgttcgaa 960
 gctgtctacg ccctcatcaa gaaccggatc caccgcctgc cggctctgga ccctgtctcc 1020

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ggggctgtgc tccacatcct cacacataag cggcttctca agttcctgca catctttggc 1080
accctgctgc cccggccctc cttcctctac cgcaccatcc aagatttggg catcggcaca 1140
ttccgagact tggccgtggt gctggaaacg gcgcccaccc tgaccgcact ggacatcttc 1200
gtggaccggc gtgtgtctgc gctgcctgtg gtcaacgaaa ctggacaggt agtgggcctc 1260
tactctcgct ttgatgtgat ccacctggct gcccaacaaa catacaacca cctggacatg 1320
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gactcactgt gggaccactg ctttgtccca ttctcagctg aaatgatgga gggcctcata 1860
agaggggtgg acaggggcctg gagtagaggc cagatcagtg acgtgccttc aggacctccg 1920
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<210> 32

<211> 514

<212> PRT

<213> Sus scrofa

<400> 32

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Met Glu Leu Ala Glu Leu Glu Gln Ala Leu Arg Arg Val Pro Gly Ser
  1              5              10              15

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Arg Gly Gly Trp Glu Leu Glu Gln Leu Arg Pro Glu Gly Arg Gly Pro
      20              25              30

```

```

Thr Thr Ala Asp Thr Pro Ser Trp Ser Ser Leu Gly Gly Pro Lys His
    35              40              45

```

```

Gln Glu Met Ser Phe Leu Glu Gln Gly Glu Ser Arg Ser Trp Pro Ser
    50              55              60

```

```

Arg Ala Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn
    65              70              75              80

```

```

Lys Ala Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro
      85              90              95

```

```

Pro Gly Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr
    100              105              110

```

```

Gly Gln Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala
    115              120              125

```

```

Pro Leu Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro
    130              135              140

```

```

Ser Asp Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp
    145              150              155              160

```

```

Leu Gly Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly
    165              170              175

```

Leu Val Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu
 180 185 190
 Pro Arg Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val
 195 200 205
 Tyr Met His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr
 210 215 220
 Ser Ser Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala
 225 230 235 240
 Phe Phe Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp
 245 250 255
 Ser Lys Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile
 260 265 270
 Leu Val Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu
 275 280 285
 Ile Glu Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly
 290 295 300
 Cys Phe Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu
 305 310 315 320
 Ala Val Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu
 325 330 335
 Asp Pro Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu
 340 345 350
 Leu Lys Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe
 355 360 365
 Leu Tyr Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu
 370 375 380
 Ala Val Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe
 385 390 395 400
 Val Asp Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln
 405 410 415
 Val Val Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln
 420 425 430
 Gln Thr Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln
 435 440 445
 Arg Thr Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr
 450 455 460
 Leu Gly Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu
 465 470 475 480

Val Leu Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser
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Asp Ile Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu
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